

Figure 1
PSSP

1	GGCAGAGCCAGCTCCTTCTGTTCCCTTGGCGGCCCTCGCTTCTTCTTCTGGATGGG	60
61	GCCCCAGGGGGCCAGGAGAGTATAAAGGCGATGTGGAGGTGCCCGGCACAACAGAGG	120
121	CCCACTCACAGGCGAGAGCCCTGGGGATGCACCGGCCAGAGGCCATGCTGCTGCTCAC	180
1	<u>M H R P E A M L L L L T</u>	12
181	GCTTGCCCTCCTGGGGGGCCCCACCTGGGCAGGGAAGATGTATGGCCCTGGAGAGGCAA	240
13	<u>L A L L G G P T W A G K M Y G P G G G K</u>	32
241	GTATTCAGCACCACCTGAAGACTACGACCATGAAATCAGGGCTGCGGGTGTCTGTAGG	300
33	Y F S T T E D Y D H E I T G L R V S V G	52
301	TCTTCTGCTGGTAAAAGTGTCCAGGTGAACTTGGAGACTCCTGGGACGTGAAACTGGG	360
53	L L L V K S V Q V K L G D S W D V K L G	72
361	AGCCTTAGGTGGGAATACCCAGGAAGTCACCCCTGCAGCCAGGCGAATACATCACAAAAGT	420
73	A L G G N T Q E V T L Q P G E Y I T K V	92
421	CTTTGTGCGCTTCCAAGCTTTCTCCGGGGTGTGGTCATGTACACCAGCAAGGACCGCTA	480
93	F V A F Q A F L R G V V M Y T S K D R Y	112
481	TTTCTATTTTGGGAAGCTTGATGGCCAGATCTCCTTGCCTACCCAGCCAAAGAGGGGCA	540
113	F Y F G K L D G Q I S S A Y P S Q E G Q	132
541	GGTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTTGGCATCAAGAGCATTTGGCTTTGA	600
133	V L V G I Y G Q Y Q L L G I K S I G F E	152
601	ATGGAATTATCCACTAGAGGAGCCGACCACTGAGCCACCAGTTAATCTCACATACTCAGC	660
153	W N Y P L E E P T T E P P V N L T Y S A	172
661	AAACTCACCGTGGGTGCTAGGGTGGGGTATGGGGCCATCCGAGCTGAGGCCATCTGGG	720
173	N S P V G R *	179
721	TGGTGGTGGCTGATGCTACTGGAGTAACTGAGTCGGGACGCTGAATCTGAATCCACCAAT	780
781	AAATAAAGCTTCTGCAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	825

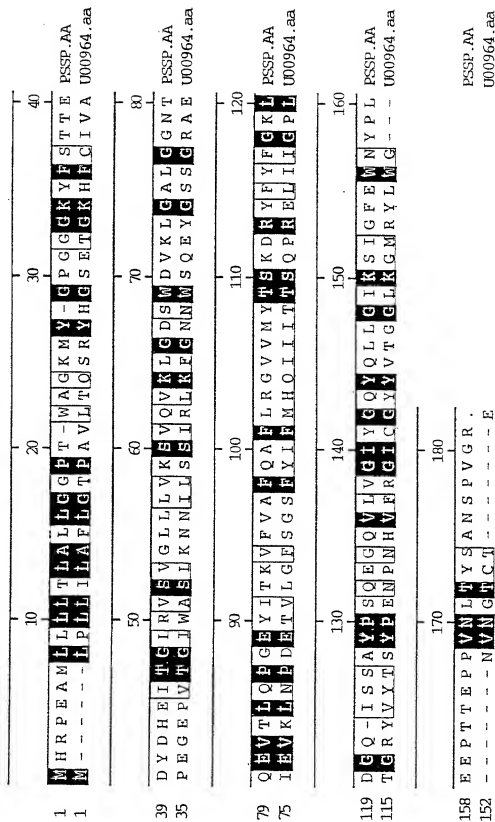


Figure 3

